

| | | |
|---|-----|-------------------------------|
| H | | gagtctaacacggaccaaggagttttaac |
| M | -60 | tgaaaagatagaataaatggcctcgtgc |
| H | | M E W P A R L C G |
| | | ATGGAGTGGCCGGCGCGGCTCTGCGGGC |
| | | * * * * |
| M | 1 | ATGGCGCGGCCAGCGCTGCTGGGCGAGC |
| M | 1 | M A R P A L L G E |
| H | | G G G G A P T E T |
| H | | GGGGGCGGGGGCGCGCCTACGGAAACTC |
| | | * * * * |
| M | 61 | GGCCAAGTTGCCGCGGCCACAGAAGTTC |
| M | 21 | G Q V A A A T E V |
| H | | E N L C T V I W T |
| H | | GAAAACCTCTGCACAGTAATATGGACAT |
| | | * * * * * * * |
| M | 121 | GAAAATCTCTGCACGATAATATGGACGT |
| M | 41 | E N L C T I I W T |
| H | | S L W Y F S H F G |
| H | | AGTCTATGGTATTTTAGTCATTTTGGCG |
| | | * * * * * |
| M | 181 | ACTCTCAGATATTTTAGTCACTTTGATG |
| M | 61 | T L R Y F S H F D |

Fig. 7A

```

acgtgcggccgggttcgagggcgagaggctgc
      . . . . .
cgaattcggcacgagccgagggcgagggcctgc

L  W  A  L  L  L  C  A  G  G  G  G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC
*      *      *      *
TGTGTTGGTGCTGCTACTGTGGACCGCCACCGTG - - -
L  L  V  L  L  L  W  T  A  T  V  -

Q  P  P  V  T  N  L  S  V  S  V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
*  *  *  *  *  *  *  *  *  *  *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q  P  P  V  T  N  L  S  V  S  V

W  N  P  P  E  G  A  S  S  N  C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
*      *  *  *  *  *  *      *  *
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W  S  P  P  E  G  A  S  P  N  C

D  K  Q  D  K  K  I  A  P  E  T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
*      *  *  *  *  *  *  *  *
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D  Q  Q  D  K  K  I  A  P  E  T
    
```

Fig. 7B

A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
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| | | | | | | | | | | |
|---|-----|------------------------------|---|---|---|---|---|---|---|---|
| H | | R | R | S | I | E | V | P | L | N |
| H | | CGTCGTTCAATAGAAGTACCCCTGAATG | | | | | | | | |
| | | * | | * | | * | * | | | |
| M | 241 | CATCGTAAAGAGGAATTACCCCTGGATG | | | | | | | | |
| M | 81 | H R K E E L P L D | | | | | | | | |
| H | | S | T | N | E | S | E | K | P | S |
| H | | AGCACCAATGAGAGTGAGAAGCCTAGCA | | | | | | | | |
| | | * | * | * | * | * | * | * | * | * |
| M | 301 | AGTGCCAATGAAAGTGAGAAGCCTAGCC | | | | | | | | |
| M | 101 | S A N E S E K P S | | | | | | | | |
| H | | G | D | P | E | S | A | V | T | E |
| H | | GGTGATCCTGAGTCTGCTGTGACTGAAC | | | | | | | | |
| | | * | * | * | * | * | * | * | * | * |
| M | 361 | GGTGATCCTGAGTCCGCTGTGACTGAGC | | | | | | | | |
| M | 121 | G D P E S A V T E | | | | | | | | |
| H | | K | C | S | W | L | P | G | R | N |
| H | | AAGTGTTCTTGGCTCCCTGGAAGGAATA | | | | | | | | |
| | | * | * | * | * | * | * | * | * | * |
| M | 421 | AAGTGTTCTTGGCTCCCTGGAAGGAATA | | | | | | | | |
| M | 141 | K C S W L P G R N | | | | | | | | |
| H | | W | H | R | S | L | E | K | I | H |
| H | | TGGCACAGAAGCCTGGAAAAAATTCATC | | | | | | | | |

Fig. 7C

E R I C L Q V G S Q C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
* * * * *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

I L V E K C I S P P E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
* * * * *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P L V K K C I S P P E

L Q C I W H N L S Y M
TTCAATGCATTTGGCACAACCTGAGCTACATG
* * * * *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M

T S P D T N Y T L Y Y
CCAGTCCCGACACTAATACTCTCTACTAT
* * * * *
CAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7D

| | | | | | | | | | |
|---|-----|-------------------------------|---|---|---|---|---|---|---|
| | | | * | | * | * | * | * | |
| M | 481 | TGGTACAGCAGCCTGGAGAAAAGTCGTC | | | | | | | |
| M | 161 | W Y S S L E K S R | | | | | | | |
| H | | F G C S F D L T K | | | | | | | |
| H | | TTTGGTTGTTTCCTTTGATCTGACCAAAG | | | | | | | |
| | | | * | * | * | | * | * | * |
| M | 541 | ATTGCTTGTTTCCTTTAAATTGACTAAAG | | | | | | | |
| M | 181 | I A C S F K L T K | | | | | | | |
| H | | Q I M V K D N A G | | | | | | | |
| H | | CAAATAATGGTCAAGGATAATGCAGGAA | | | | | | | |
| | | | * | * | * | * | * | * | * |
| M | 598 | CAAATAATGGTCAAGGATAATGCTGGGA | | | | | | | |
| M | 200 | Q I M V K D N A G | | | | | | | |
| H | | T S R V K P D P P | | | | | | | |
| H | | ACTTCCC GTGTGAAACCTGATCCTCCAC | | | | | | | |
| | | | * | * | | * | * | * | * |
| M | 658 | ACTTCCTATGTGAAACCTGATCCTCCAC | | | | | | | |
| M | 220 | T S Y V K P D P P | | | | | | | |
| H | | L Y V Q W E N P Q | | | | | | | |
| H | | CTATATGTGCAATGGGAGAATCCACAGA | | | | | | | |
| | | | * | * | * | * | * | * | * |
| M | 718 | TTATTAGTGCAGTGGAAGAATCCACAAA | | | | | | | |
| M | 240 | L L V Q W K N P Q | | | | | | | |

Fig. 7E

* * * * *

AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

V K D S S F E Q H S V
TGAAGGATTCCAGTTTGAACAACACAGTGTC
* * * *

TGGAACCT- - -AGTTTTGAACATCAGAACG TT
V E P - S F E H Q N V

K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * *

AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K I R P S C K I V S L

H I K N L S F H N D D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
* * * *

ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A

N F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * *

ATTTTAGAAGCAGATGCTTA ACTTATGAAGTG
N F R S R C L T Y E V

Fig. 7F

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| | | | | | | | | | | |
|---|-----|-------------------------------|---|---|---|---|---|---|---|---|
| H | | E | V | N | N | S | Q | T | E | T |
| H | | GAAGTCAATAACAGCCAAACTGAGACAC | | | | | | | | |
| | | * | * | * | * | | * | * | | |
| M | 778 | GAGGTCAATAATACTCAAACCGACCGAC | | | | | | | | |
| M | 260 | E | V | N | N | T | Q | T | D | R |
| H | | E | N | P | E | F | E | R | N | V |
| H | | GAGAATCCAGAAATTTGAGAGAAATGTGG | | | | | | | | |
| | | * | | * | | | * | * | | |
| M | 838 | CAGAATTCCGAATCTGATAGAAACATGG | | | | | | | | |
| M | 280 | Q | N | S | E | S | D | R | N | M |
| H | | L | P | D | T | L | N | T | V | R |
| H | | CTTCCTGATACTTTGAACACAGTCAGAA | | | | | | | | |
| | | * | | * | | | * | * | * | |
| M | 898 | CTTGCCGACGCTGTCTACACAGTCAGAG | | | | | | | | |
| M | 300 | L | A | D | A | V | Y | T | V | R |
| H | | D | D | K | L | W | S | N | W | S |
| H | | GATGACAAACTCTGGAGTAATTGGAGCC | | | | | | | | |
| | | * | | * | * | * | * | | * | * |
| M | 958 | GACAACAAACTGTGGAGTGATTGGAGTG | | | | | | | | |
| M | 320 | D | N | K | L | W | S | D | W | S |
| H | | T | L | Y | I | T | M | L | L | I |
| H | | AACTCTACATAACCATGTTACTCATTG | | | | | | | | |

Fig. 7G

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H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C

E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S

V P V I V A G A I I V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig. 7H

A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
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REPLACEMENT SHEET

| | | | | | | | | | | | | | |
|---|------|--|---|---|---|---|---|---|---|---|---|---|---|
| | | | * | | * | | * | | * | | * | | * |
| M | 1018 | | A | C | C | T | T | C | T | A | C | A | C |
| M | 340 | | T | F | Y | T | T | M | L | L | T | | |
| H | | | L | L | L | Y | L | K | R | L | K | | |
| H | | | C | T | C | T | G | C | T | T | A | C | T |
| | | | | | | | | | | | | | |
| | | | * | | * | | * | | * | | * | | * |
| M | 1078 | | C | T | C | T | T | T | A | C | T | G | A |
| M | 360 | | L | L | F | Y | L | K | R | L | K | | |
| H | | | K | I | F | K | E | M | F | G | D | | |
| H | | | A | A | G | A | T | T | T | T | A | A | G |
| | | | | | | | | | | | | | |
| | | | * | | * | | * | | * | | * | | * |
| M | 1138 | | A | A | G | A | T | T | T | T | A | A | G |
| M | 380 | | K | I | F | K | E | M | F | G | D | | |
| H | | | D | I | Y | E | K | Q | T | K | E | | |
| H | | | G | A | C | A | T | C | T | A | T | G | A |
| | | | | | | | | | | | | | |
| | | | * | | * | | * | | * | | * | | * |
| M | 1198 | | G | A | C | A | T | C | T | A | T | G | A |
| M | 400 | | D | I | Y | E | K | Q | S | K | E | | |
| H | | | K | K | A | S | Q | * | | | | | |
| H | | | A | A | G | A | G | C | C | T | C | T | C |
| | | | | | | | | | | | | | |
| | | | * | | * | | * | | | | | | |
| M | 1258 | | A | A | G | A | G | C | A | G | C | T | C |
| M | 420 | | K | K | A | A | P | * | | | | | |

Fig. 7I

```

      *   *       *   *       *       *
TTCCAGTCTTTGTCGCGAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I

I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*   *   *   *   *   *   *   *   *   *
TCATTATATTTCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G

Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y

E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*   *   *   *   *   *   *   *   *   *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L

ttatTTTTaccttcactgtgaccttgagaaga
tgatttctttcttgccttcaatgtgaccctgt
    
```

Fig. 7J